A functional screen of translated pancreatic IncRNAs identifies a microprotein-independent role for LINC00261 in endocrine cell differentiation

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Graphical Abstract

Human pancreas development

hESCs

Dynamically expressed IncRNAs

Transcribed

Translated + 25%

Endocrine cells

Translated IncRNA CRISPR LoF screen

LINC00261 microproteins not functionally required

Fewer insulin+ endocrine cells

Highlights

• Extensive IncRNA translation and microprotein production during human pancreas development
• A small-scale loss-of-function screen shows most translated IncRNAs are dispensable
• LINC00261 is highly translated and regulates endocrine cell differentiation
• Deleting LINC00261’s evolutionary young microproteins reveals no essential roles

Abstract

Long noncoding RNAs (IncRNAs) are a heterogeneous group of RNAs, which can encode small proteins. The extent to which developmentally regulated IncRNAs are translated and whether the produced microproteins are relevant for human development is unknown. Here, we show that many IncRNAs in direct vicinity of lineage-determining transcription factors (TFs) are dynamically regulated, predominantly cytosolic, and highly translated during pancreas development. We genetically ablated ten such IncRNAs, most of them translated, and found that nine are dispensable for endocrine cell differentiation. However, deletion of LINC00261 diminishes generation of insulin+ endocrine cells, in a manner independent of the nearby TF FOXA2. Systematic deletion of each of LINC00261’s seven poorly conserved microproteins shows that the RNA, rather than the microproteins, is required for endocrine development. Our work highlights extensive translation of IncRNAs into recently evolved microproteins during human pancreas development and provides a blueprint for dissection of their coding and noncoding roles.
INTRODUCTION

Defects in pancreatic endocrine cell development confer increased diabetes risk later in life (Bakhti et al., 2019). Therefore, a detailed understanding of the factors that orchestrate endocrine cell differentiation is highly relevant to human disease. Many of the molecular mechanisms that underlie the formation of pancreatic endocrine cells have been defined (Schiesser & Wells, 2014; Romer & Sussel, 2015), but a thorough functional assessment of the noncoding transcriptome, and in particular that of long noncoding RNAs (lncRNAs), is currently lacking.

Most lncRNAs with to date demonstrated roles in the regulation of fundamental developmental processes are active in the cell’s nucleus (Klattenhoff et al., 2013; Lin et al., 2014; Jiang et al., 2015; Kurian et al., 2015; Ramos et al., 2015; Daneshvar et al., 2016; Luo et al., 2016). However, a large proportion of lncRNAs is predominantly randomly distributed in the genome but frequently located noncoding classification of lncRNAs, emphasizing the need for a thorough functional assessment of the noncoding RNAs (lncRNAs) possesses short, “non-canonical” open reading frames (sORFs) that are actively translated (Bazzini et al., 2014; Ruiz-Orera et al., 2014; Makarewich & Olson, 2017).

Although most of these non-canonical ORFs produce microproteins that are poorly conserved across species, recent studies have systematically assessed their biological activity, revealing roles across cellular organelles and, for a subset of microproteins, essential functions for cell survival (van Heesch et al., 2019; Chen et al., 2020; Persnser et al., 2020). This previously unrecognized coding capacity of supposedly noncoding RNAs has called into question the noncoding classification of lncRNAs, emphasizing the need for careful dissection of any gene’s coding and noncoding functions.

LncRNAs, whether translated or fully noncoding, are not randomly distributed in the genome but frequently located close to, and coregulated with, canonical protein-coding genes in cis (Luo et al., 2016; Neumann et al., 2018; van Heesch et al., 2019). For example, the lncRNAs DIGIT (also known as GSC-DT) and Gata6as (also known as IncGata6 or GATA6-AS1) have been reported to enhance expression of the divergently expressed endoderm regulators Goosecoid (GSC) and Gata6, respectively (Daneshvar et al., 2016; Luo et al., 2016; Neumann et al., 2018). Similarly, LINC00261 (also known as DEANR1) and its neighboring transcription factor (TF) FOXA2 are both induced in endoderm formation, during which LINC00261 has been demonstrated to positively regulate FOXA2 expression (Jiang et al., 2015). However, whether such cis-acting lncRNAs are translated and may exert cytosolic functions through trans-acting, microprotein-dependent mechanisms relevant for endoderm and pancreas development is not known.

In this study, we newly identify actively translated lncRNAs and analyze their role in human pancreas development. We accomplished this by classifying lncRNAs based on their dynamic regulation, subcellular localization, and active translation during the stepwise differentiation of human embryonic stem cells (hESCs) toward the pancreatic fate. We used this classification to prioritize select dynamically regulated and highly translated lncRNAs for deletion in hESCs, followed by extensive phenotypic characterization across multiple intermediate stages of pancreas development. This small-scale loss-of-function screen reveals that nine out of the ten selected lncRNAs are not essential for pancreatic development and, despite their vicinity to lineage-determining TFs, none of these lncRNAs regulate the expression of these TFs in cis.

The deletion of one lncRNA, LINC00261, does impair human endocrine cell development and leads to a significant reduction in the number of insulin-producing cells. Contrary to previous studies of LINC00261 knockout hESCs (Jiang et al., 2015), deletion of LINC00261 has no effect on the expression of nearby TF FOXA2 or other proximal genes, suggesting control of endocrine cell formation through a trans- rather than cis-regulatory mechanism. LINC00261 is one of the most highly translated lncRNAs based on ribosome profiling (Ribo-seq) and produces multiple microproteins with distinct subcellular localizations. To systematically assess LINC00261’s coding and noncoding functions, we separately introduced frame shift mutations into each of seven identified LINC00261 sORFs. However, rigorous phenotypic characterization revealed no apparent consequences of loss of each of the seven LINC00261-sORF-encoded microproteins on endoderm cell development. Our comprehensive assessment of functional lncRNA translation identifies a microprotein-independent trans-regulatory role for LINC00261 in endocrine cell differentiation and provides a blueprint for the proper dissection of a gene’s coding and noncoding roles in a human disease-relevant system.

RESULTS

LncRNAs and nearby lineage-determining transcription factors exhibit dynamic coregulation during pancreas development

To identify lncRNAs involved in the regulation of pancreas development, we profiled RNA expression at five defined stages of hESC differentiation toward the pancreatic lineage: hESCs (ES), definitive endoderm (DE), primitive gut tube (GT), early pancreatic progenitor (PP1), and late pancreatic progenitor (PP2) (Figure 1A). While some lncRNAs were constitutively expressed (n = 592; 25.3%), the majority showed dynamic expression patterns, being either strongly enriched in (n = 874; 37.4%), or specific to (n = 871; 37.3%) a single developmental intermediate of pancreatic lineage progression (Figure 1B and Table S1A). The expression of many of these dynamically regulated lncRNAs correlated with that of proximal coding genes (Figure S1A-D and Table S1B,C), further exemplified by a subset of lncRNAs that was specifically coregulated with the key endodermal and pancreatic TFs GATA6, FOXA2, PDX1, and SOX9 (Figure 1C,D). The tight expression coregulation of these IncRNA-TF pairs is likely explained by a shared chromatin environment (Figure S1E-H), which raises the possibility that like the TFs, the function of the lncRNAs is also required for endoderm and pancreas development.

Many pancreatic progenitor-expressed lncRNAs are cytoplasmically enriched and translated

Although most functional roles described for lncRNAs to date have been predominantly nuclear (Marchese et al., 2017), multiple recent studies have shown that many lncRNAs are cytosolic and actively translated into sometimes biologically active microproteins (Makarewich & Olson, 2017). To further characterize the above-identified dynamically regulated lncRNAs, we analyzed their subcellular localization and translation potential.
using fractionation RNA-seq and Ribo-seq (Figure 2A). Of all lncRNAs expressed in pancreatic progenitor cells (PP2 cells), we classified 21% (n = 347) as localized to the nucleus, whereas a larger number (n = 563; 34%) primarily resided in the cytosol (Figure S2A and Table S2A). This subcellular distribution of pancreatic IncRNAs is in agreement with previous IncRNA localization studies by us and others (Clark et al., 2012; van Heesch et al., 2014; Cabili et al., 2015; Sun et al., 2015). LncRNAs enriched in the cytosol were expressed at higher levels than nucleus-localized IncRNAs, with expression levels similar to canonical protein-coding mRNAs (Figure S2B). Intriguingly, almost half of all cytoplasmic IncRNAs (278 out of 563; 49.4%) displayed dynamic expression regulation during the differentiation of hESCs to pancreatic progenitors, suggesting that many IncRNAs with putative developmental functions do not act in the nucleus, but instead in the cytosol where they may be translated.

To investigate the translation potential of these cytosolic IncRNAs, we used Ribo-seq, obtaining exceptionally deep and high quality translatome coverage across six replicate differentiations (Figure S2C and Table S2B). As nearly 90% of the sequenced ribosomal footprints exhibited clear 3-nucleotide codon movement characteristic of active translation (Figure S2D-F), these data have strong predictive value for the computational detection of non-canonical ORFs in IncRNAs (Table S2C). Requiring stringent reproducibility criteria (the exact ORF needed to be detected by RiboTaper (Calviello et al., 2016) in at least four out of the six replicates), we identified a total of 625 new sORFs in IncRNAs with a median length of 47 amino acids (aa) (Table S2D). The majority of detected sORFs (76%; n = 477/625) is currently not present in the sORFs.org database (Olexiouk et al., 2016) and thus completely novel. The translated sORFs are located within 285 cytosolically localized IncRNAs (25.3% of all expressed IncRNAs) (Figure S2B), which are expressed at higher levels than untranslated IncRNAs (Figure S2G and Table S2E).

Of note, only few of the newly identified sORFs are highly conserved across species, as judged by their low PhyloCSF scores (Lin et al., 2011) (Table S2D). However, the relevance of our ORF detection approach and the importance of lowly conserved ORFs for human biology have recently been demonstrated by several independent studies, focusing on either cardiac biology (van Heesch et al., 2019) or human cancer cell survival (Chen et al., 2020; Prensner et al., 2020). To our knowledge, our data constitute the first comprehensive set of non-canonical
Figure 2. Cytosolic lncRNAs contain translated small open reading frames.

(A) Overview of experimental strategy for subcellular fractionation and Ribo-seq-based identification of translated small open reading frames (sORFs) from lncRNAs expressed in PP2 cells. Replicates from six independent differentiations to the PP2 stage each for total (polyA) RNA-seq and Ribo-seq experiments, and two biological replicates for the subcellular fractionation were analyzed. The histogram on the far right depicts the size distribution of the sORF-encoded small peptides as number of amino acids (aa). The pie chart summarizes the percentages of constitutively and dynamically expressed sORF-encoding lncRNAs during pancreatic differentiation of CyT49 hESCs.

(B-E) Left: Bar graphs showing nuclear and cytosolic expression (in RPKM) of lncRNAs **RP11-834C11.4** (B), **LINC00261** (C), **MIR7-3HG** (D). Right: Fluorescence microscopy images showing expression of modified lncRNAs with sORFs in CyT49 hESCs.
human ORFs generated from a non-transformed human cell model of development, providing a valuable resource for future functional studies.

**Transcribed pancreatic IncRNAs produce microproteins with distinct subcellular localizations**

Having established that many stage-specific pancreatic IncRNAs are actively translated, we next sought to validate their translation potential through independent experimental approaches, and to demonstrate production of the predicted microproteins at the protein level. To this end, we first performed coupled in vitro transcription/translation assays on endogenous and complete transcript isoforms of four of the most highly transcribed IncRNAs (LINC00261, RP11-834C11.4, LHFPL3-AS2, and MIR7-3HG; Figure S2I; expression and ORF information in Figure 2B-E). Second, we generated a series of in vivo translation reporter constructs to assess the subcellular localization of microproteins translated from each of ten sORFs derived from the same four IncRNAs. Transient expression of individual constructs carrying in-frame GFP fusions in HEK293T cells produced GFP signal for all ten assayed microproteins, which was abolished upon introduction of a frameshift within the sORF or a stop codon following the sORF sequence (Figure 2F and Figure S2J-L). To rule out a possible localization bias induced by the GFP fusion, we also expressed a FLAG-tag fusion peptide (RP11-834C11.4 sORF-1×FLAG), which revealed a cytoplasmic localization identical to the one observed for the GFP construct (Figure S2J). While most sORF-GFP fusion products were ubiquitously distributed throughout transfected cells, LINC00261 sORF-4 GFP specifically localized to mitochondria (Figure S2K), and LINC00261 sORF-7 GFP exhibited a perinuclear accumulation pattern reminiscent of aggresomes (Figure S2L). Taken together, our results validate the translation potential of sORFs encoded by pancreatic progenitor-expressed IncRNAs and show that these translation events result in robust production of microproteins with different subcellular localizations.

**Systematic knockout of translated IncRNAs during pancreas development**

To identify potential functional roles of translated IncRNAs and the microproteins they produce in pancreas development, we selected ten candidates for CRISPR/Cas9-based genome editing in hESCs through excision of the IncRNA promoter or entire IncRNA locus (Figure 3A,B). These ten IncRNAs were prioritized based on (i) high expression and endodermal tissue-specificity, (ii) dynamic regulation during pancreas development, (iii) abundant translation of sORFs, and (iv) proximity to TFs with known roles in endoderm and pancreas development. For seven of the selected IncRNAs, translation was highly abundant and reproducibly detected across Ribosome-seq replicates: LINC00617 (also known as TUNAR; [Lin et al., 2014]), GATA6-AS1 (also known as GATA6-AS; [Neumann et al., 2018]), LINC00261, RP11-834C11.4, SOX9-AS1, MIR7-3HG, and LHFPL3-AS2. Although for two additional IncRNAs the translation potential could not be determined, they were nonetheless included because of a previously reported requirement for definitive endoderm formation (DIGIT, also known as GSC-DT) ([Daneshvar et al., 2016]) and genomic localization adjacent to the definitive endoderm TF LHX1 (RP11-445F12.1, also known as LHX1-DT). Lastly, LINC00479 was chosen as a non-translated control with expression dynamics and a subcellular localization similar to LINC00261. Of note, for each of the ten selected IncRNAs, we generated at least two independent hESC knockout (KO) clones and used different combinations of single guide RNAs where possible (Table S3A).

We next differentiated each of the IncRNA KO hESC lines stepwise toward the pancreatic endocrine cell stage, conducting up to 16 replicate differentiations per clone. Because LINC00617, RP11-445F12.1, DIGIT, GATA6-AS1, LINC00479, and LINC00261 were first expressed at, or before, the definitive endoderm stage (Figure 3A), we determined whether KO hESCs for these IncRNAs exhibited defects in definitive endoderm formation. Despite efficient IncRNA depletion (Figure S3A,B), neither quantification of definitive endoderm marker gene expression by qRT-PCR, nor immunofluorescence staining or flow cytometric analysis of the definitive endoderm marker SOX17 showed differences indicative of impaired endoderm formation in IncRNA KO lines (Figure 3C-E). Importantly, expression of TFs located in the direct vicinity of these IncRNAs, including GSC (DIGIT), LHX1 (RP11-445F12.1), GATA6 (GATA6-AS1), and FOXA2 (LINC00261), was unaffected by the IncRNA KO (Figure 3F, Figure S3C, Table S3B-D), arguing against cis-regulation by these IncRNAs. These findings are in contrast to prior reports that have shown a requirement for LINC00261 and DIGIT in definitive endoderm formation and the regulation of neighboring TFs FOXA2 and GSC, respectively ([Jiang et al., 2015]; Daneshvar et al., 2016; Amaral et al., 2018; Swarr et al., 2019]).

Next, we further differentiated control and KO lines for eight out of ten IncRNAs toward the endocrine cell stage, excluding DIGIT and RP11-445F12.1 because they are not expressed after the definitive endoderm stage (Figure 3A). In KO hESC lines of seven out of these eight IncRNAs, we observed no effect on pancreatic progenitor cell formation or gene expression, with the exception of a few dysregulated genes in LHFPL3-AS2 and RP11-834C11.4 KO cells (Figure S3C and Table S3E-K). Furthermore, deletion of neither of the seven IncRNAs impaired endocrine cell formation, as determined by quantification of insulin+ cells and insulin mRNA levels (Figure 3G-I). Similar to the RNA expression results obtained at the definitive endoderm stage, deletion of none of the IncRNAs close to pancreatic TFs (e.g. GATA6-AS1 and SOX9-AS1) altered the expression of these TFs, once more arguing against cis-regulation of these TFs by the neighboring IncRNA (Figure S3C).
Figure 3. A small-scale CRISPR loss-of-function screen for dynamically expressed and translated lncRNAs during pancreatic differentiation.

(A) qRT-PCR analysis of candidate lncRNAs during pancreatic differentiation of H1 hESCs relative to the ES stage. Data are shown as mean ± S.E.M. (mean of n = 2-6 independent differentiations per stage; from H1 hESCs).

(B) CRISPR-based lncRNA knockout (KO) strategy in H1 hESCs and subsequent phenotypic characterization.

(C) Immunofluorescence staining for OCT4 and SOX17 in DE from control (ctrl) and KO cells for the indicated lncRNAs (representative images, n ≥ 3 independent differentiations; at least two KO clones were analyzed).

(D) qRT-PCR analysis of DE lineage markers in DE from control and lncRNA KO (-/-) cells. TF genes in cis to the lncRNA locus are highlighted in red. Data are shown as mean ± S.E.M. (n = 3-16 replicates from independent differentiations and different KO clones). NS, p-value > 0.05; t-test.

(E) Flow cytometry analysis at DE stage for SOX17 in control and KO (-/-) cells for indicated lncRNAs. The line demarks isotype control. Percentage of cells expressing SOX17 is indicated (representative experiment, n ≥ 3 independent differentiations from at least two KO clones).

(F) Immunofluorescence staining for FOXA2 or GATA6 in DE from control and KO (LINC00261, GATA6-AS1, and DIGIT KO cells).

(G) Immunofluorescence staining for insulin (INS) in endocrine cell stage (EC) from control and KO
hESCs for the indicated lncRNAs (representative images, n ≥ 3 independent differentiations from at least two KO clones). (H) qRT-PCR analysis of INS in EC stage cultures from control and IncRNA KO (-/-) hESCs. Data are shown as mean ± S.E.M. (n ≥ 4 replicates from independent differentiations of at least two KO clones). NS, p-value > 0.05; t-test. (I) Flow cytometry analysis at EC stage for INS in control and KO (-/-) cells for indicated IncRNAs. The line demarks isotype control. Percentage of cells expressing insulin is indicated from independent differentiations of at least two KO clones). Scale bars = 100 µm. See also Figure S3 and Table S3.

Thus, nine out of ten endoderm- and pancreatic progenitor-enriched IncRNAs functionally investigated here appear to be nonessential for induction of the pancreatic fate and formation of insulin+ cells. Furthermore, these IncRNAs do not control the transcription of their proximal TFs.

**LINC00261** knockout impairs endocrine cell development

The exception is the endoderm-specific IncRNA LINC00261, which is highly expressed and translated in pancreatic progenitors (Figure S4A and Figure 2C). While deletion of LINC00261 caused no discernable phenotype in definitive endoderm (Figure 3C-F and Figure S3C), we observed a significant 30-50% reduction in the number of insulin+ cells at the endocrine cell stage (Figure 4A,B). This reduction in insulin+ cell numbers was consistent across four independently derived LINC00261 KO hESC lines. In agreement with the reduced insulin+ cell numbers, insulin content and insulin mRNA levels were also reduced in LINC00261 KO endocrine stage cultures (Figure 4C,D). Analysis of insulin fluorescence intensities by flow cytometry further showed no reduction in insulin levels per cell in one LINC00261 KO clone and a mild reduction in the three other clones (Figure 4E), demonstrating that LINC00261 predominately regulates endocrine cell differentiation rather than maintenance of insulin production in beta cells.

To determine the molecular effects of LINC00261 deletion, we performed RNA-seq in pancreatic progenitors derived from LINC00261 KO and control hESCs. Among the down-regulated genes were the TFs MAFB and PAX4 (Figure 4F, Figure S4B, Table S4A), which are important regulators of beta cell differentiation (Sosa-Pineda et al., 1997; Artner et al., 2007). Similar to the absence of cis-regulatory functions observed in the other IncRNA KO lines, we found no evidence for cis-regulation of FOXA2 by LINC00261 (Figure 4F and Figure S4C). Of note, the genes differentially expressed in LINC00261 KO cells mapped to all chromosomes and showed no enrichment for chromosome 20 where LINC00261 resides (Figure 4G). Combined, our results suggest a trans- rather than cis-regulatory function for LINC00261, consistent with its predominantly cytosolic localization, active translation, and diffuse distribution within the nucleus (Figure 2C and Figure S4D). This potential trans functionality prompted us to further investigate whether LINC00261’s coding or noncoding features are essential for endocrine cell differentiation.

The **LINC00261** transcript, and not the encoded microproteins, is required for endocrine cell differentiation

We established that LINC00261 harbors multiple distinct and highly translated sORFs, which produce poorly conserved microproteins with diverse subcellular localizations (Figure 2C,F, Figure S2L,K,L, Table S2D). This raises the possibility that LINC00261-sORF-encoded microproteins, and not the RNA itself, are functionally important for endocrine cell differentiation. To systematically dissect whether the microproteins are required for endocrine cell formation independent of LINC00261 RNA, we individually mutated all seven sORFs in independent hESC lines, leaving the IncRNA sequence grossly intact. Each of these hESC lines either carries a homozygous frameshift mutation near the microprotein’s N-terminus (for sORFs 1-6) or a full sORF deletion (sORF7; Table S4B). After verifying that CRISPR editing of the LINC00261 locus did not impact LINC00261 transcript levels (Figure S4E), we quantified (i) insulin mRNA levels, (ii) insulin+ cells, and (iii) total insulin content in endocrine cell stage cultures. We observed no difference between sORF loss-of-function and control hESC lines for any of these endpoints (Figure 4H,I and Figure S4E). Consistently, transcriptome analysis of pancreatic progenitors with frameshifts in sORF3 (the most highly translated LINC00261-sORF; Figure 2C and Table S2D) revealed no differentially expressed genes between LINC00261-sORF3 frameshift and control cells (Figure 4J and Table S4C), contrasting observations in LINC00261 RNA KO pancreatic progenitors (Figure 4F and Table S4A).

It has been suggested that ribosome association can degrade IncRNAs, e.g., through nonsense-mediated decay (Tani et al., 2013; Carlevaro-Fita et al., 2016). Therefore, to determine whether the multiple sORFs within LINC00261 regulate LINC00261 stability, we simultaneously mutated start codons of all seven sORFs (∆ATG×sORF1-7 LINC00261) and expressed either wild type or ∆ATG×sORF1-7 LINC00261 ectopically in HEK293T cells where LINC00261 is normally not expressed. LINC00261 half-life measurements upon transcriptional inhibition with actinomycin D revealed no difference in LINC00261 levels between wild type and ∆ATG×sORF1-7 LINC00261 (Figure 4K), suggesting that the association of LINC00261 with ribosomes does not affect its stability.

In sum, through the systematic, one-by-one removal of microproteins produced from a highly translated IncRNA with functional importance for pancreatic endocrine cell formation, we found no evidence to implicate the individual microproteins in endocrine cell development. Although LINC00261’s microproteins may share functional redundancy or have developmental roles that do not affect the production of insulin+ cells, our findings strongly suggest that by themselves, each of the LINC00261-sORF-encoded microproteins is not functionally required for endocrine cell formation.

**DISCUSSION**

The highly translated IncRNA LINC00261 is a novel regulator of endocrine cell differentiation

In this study, we globally characterized molecular features of IncRNAs expressed during progression of hESCs toward the pancreatic lineage, including their subcellular localization and potential to be translated and to produce microproteins. We performed a phenotypic CRISPR loss-of-function screen, focusing on ten developmentally regulated, highly expressed, and highly translated IncRNAs proximal to TFs known to regulate pancreas development.
Figure 4. *LINC00261* deletion impedes pancreatic endocrine cell differentiation.

(A) Flow cytometry analysis at endocrine cell stage (EC) for insulin (INS) in control (ctrl) and *LINC00261*−/− H1 hESCs. Top panel: Schematic of the *LINC00261* locus. The dashed box represents the genomic deletion. Middle panel: The line demarks isotype control. Percentage of cells expressing INS is indicated (representative experiment, n = 4 deletion clones generated with independent sgRNAs). Bottom panel: Bar graph showing percentages of INS-positive cells. Data are shown as mean ± S.D. (n = 5 (clone 1), n = 6 (clone 2), n = 8 (clone 3), n = 5 (clone 4) independent differentiations).

(B) Immunofluorescence staining for INS in EC stage cultures from control and *LINC00261*−/− hESCs (representative images, number of differentiations see A).

(C) ELISA for INS in EC stage cultures.
from control and LINC00261-/- hESCs. Data are shown as mean ± S.D. (n = 3 (clone 1), n = 2 (clone 2), n = 14 (clone 3), n = 13 (clone 4) independent differentiations). (D) qRT-PCR analysis of INS in EC stage cultures from control and LINC00261-/- hESCs. Data are shown as mean ± S.E.M. (n = 8 (clone 1), n = 5 (clone 2), n = 11 (clone 3), n = 3 (clone 4) independent differentiations). (E) Quantification of median fluorescence intensity after INS staining of control and LINC00261-/- hESCs cultures. Data are shown as mean ± S.D. (n = 5 (clone 1), n = 6 (clone 2), n = 8 (clone 3), n = 5 (clone 4) independent differentiations), iso, isotype control. (F) Volcano plot displaying gene expression changes in control versus LINC00261-/- PP2 cells (n = 6 independent differentiations from all four deletion clones). Differentially expressed genes are shown in red (DESeq2: > 2-fold change (FC), adjusted p-value < 0.01) and blue (> 2-fold change, adjusted p-value ≥ 0.01 and < 0.05). (G) qRT-PCR analysis of LINC00261 in EC stage cultures from control and LINC00261-/- hESCs. Data are shown as mean ± S.D. (n = 4-7 independent differentiations per clone). (I) Volcano plot displaying gene expression changes in control versus LINC00261-/- sORF-3 FS PP2 cells. Data are shown as mean ± S.D. (n = 3-7 independent differentiations per clone). (J) Volcano plot displaying gene expression changes in control versus LINC00261-/- sORF-3 FS PP2 cells. Data are shown as mean ± S.D. (n = 2-6 independent differentiations per clone). LINC00261 is shown in gray, the bar graph insert displays LINC00261 RPKM values in control and LINC00261-/- sORF-3 FS PP2 cells. (K) LINC00261 half-life measurements in HEK293T cells transduced with lentivirus expressing either wild type (WT) LINC00261 or ΔATG LINC00261 (mutant in which the ATG start codons of sORFs 1-7 were changed to non-start codons). HEK293T were treated with the transcription inhibitor actinomycin D and RNA isolated at 0, 2, 4, 6, 8, and 9 hours post actinomycin D addition. LINC00261 expression was analyzed by qRT-PCR relative to the TBP gene. Data are shown as mean ± S.E.M. (n = 3 (clone 1), n = 2 (clone 2), n = 14 (clone 3), n = 3 (clone 4) independent differentiations). iso, isotype control.

The first important observation from this screen is that we find no evidence to implicate the IncRNAs LINC00261, DIGIT, GATA6-AS1, SOX9-AS1, and RPL11-445F12.1 in the cis-regulation of their neighboring TFs FOXA2, GSC, GATA6, SOX9, and LHX, respectively, despite tight transcriptional coregulation of the IncRNA-TF pairs.

Second, we identify the translated incRNA LINC00261 as a novel regulator of pancreatic endocrine cell differentiation, as evidenced by a severe reduction in insulin* cell numbers upon LINC00261 deletion. We show that LINC00261 transcripts are highly abundant in pancreatic progenitors and, albeit present in the nucleus, are predominantly localized to the cytoplasm. Here, they frequently associate with ribosomes to produce multiple distinct microproteins. Through the introduction of individual frameshift mutations in each of the microprotein-encoding sORFs of LINC00261, we could uncouple the requirement of LINC00261 in endocrine cell development from microprotein production. Furthermore, mutating all translated LINC00261 sORFs simultaneously and thereby significantly reducing LINC00261's ability to bind ribosomes, did not affect LINC00261 transcript levels. This indicates that, in contrast to some reports suggesting that translated sORFs can regulate RNA stability by promoting nonsense-mediated RNA decay (Tani et al., 2013; Carlevaro-Fita et al., 2016), the high translation levels and multiple sORFs of LINC00261 are not part of a LINC00261 decay pathway.

Although IncRNAs are now appreciated as a novel and abundant source of sORF-encoded biologically active microproteins (Makearewich & Olson, 2017), we found no essential roles for LINC00261-sORF-encoded microproteins in endocrine cell development. Possibly, this is explained by the fact that most microproteins - including the majority of microproteins newly identified in this study, and all microproteins produced by LINC00261 - are poorly conserved across species. Since the functional role of the vast majority of such recently evolved microproteins has not been systematically investigated, there is an ongoing debate about their significance for vital cellular processes (Ruiz-Orera et al., 2018; Levy, 2019). Recent reports, however, suggest that lowly expressed sORF-encoded microproteins can indeed have important functions in terminally differentiated cells and in cancer. (van Heesch et al., 2019; Chen et al., 2020; Prensner et al., 2020). This raises the possibility that LINC00261-sORF-encoded microproteins could possess functions that become relevant under specific environmental, developmental, or disease conditions not examined in this study.

LINC00261 - a potential trans regulator of endocrine cell differentiation?

Several lines of evidence suggest that LINC00261 regulates endocrine cell differentiation in trans: (i) LINC00261 transcripts show a diffuse distribution in multiple subcellular compartments, (ii) genes differentially expressed in LINC00261 KO cells are randomly distributed throughout the genome, (iii) expression of the nearby TF FOXA2 is not affected by LINC00261 deletion. Such a trans regulatory mechanism for LINC00261 is supported by a recent study from the GTEx Consortium, where LINC00261 is highlighted as one of a few IncRNAs that forms a potential trans regulatory hotspot through genetic interactions that influence the expression of multiple distant genes (Aguet et al., 2019). Consistent with its preferential cytosolic localization, and further supporting the notion of a trans regulatory mechanism, LINC00261 has been suggested to regulate gene expression through non-nuclear mechanisms, e.g. by preventing nuclear translocation of β-catenin (Wang et al., 2017) or by acting as a miRNA sponge (Shi et al., 2019; Wang et al., 2019; Yan et al., 2019). Although our observations and current literature strongly hint to a function in trans independent of the produced microproteins, the exact mechanism by which LINC00261 regulates gene expression in pancreatic progenitors remains to be determined.

We here present a rigorous, in-depth characterization of dynamically regulated and translated IncRNAs in a disease-relevant cell context of human developmental progression. Our combination of ultra-high-coverage RNA and Ribo-seq, protein-level validation of microprotein production and localization, and the systematic deletion of all individual microproteins encoded by a single translated IncRNA not only provides a detailed map of microprotein production and localization, but also serves as a blueprint for the systematic functional interrogation of translated IncRNAs during human organ development.
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Author Contributions


Declaration of Interests

The authors declare no competing interests.

Materials and Methods

HEK293T cell culture

HEK293T cells (female) were cultured in a humidified incubator at 37 °C with 5% CO₂ using Dulbecco’s Modified Eagle Medium (Cat# 45000-312; 4.5 g/L glucose, [+L-glutamine, [-] sodium pyruvate) supplemented with 10% fetal bovine serum (FBS).

hESC culture and maintenance

H1 hESCs (male) were grown in feeder-independent conditions on Matrigel®-coated dishes (Corning) with mTeSR1 media (STEMCELL Technologies). Propagation was carried out by passing the cells every 3 to 4 days using Accutase™ (eBioscience) for enzymatic cell dissociation. hESC research was approved by the University of California, San Diego, Institutional Review Board and Embryonic Stem Cell Research Oversight Committee.

Pancreatic differentiation

H1 hESCs were differentiated in a monolayer format as previously described (Rezania et al., 2012), with minor modifications. Undifferentiated hESCs were seeded into 24-wells at 0.4 × 10⁶ cells/well in 500 µl mTeSR1 medium. The next day the cells were washed in RPMI media (Thermo Fisher Scientific) and then differentiated with daily media changes. In addition to GlutaMAX™, RPMI medium was supplemented with 0.12% (w/v) NaHCO₃ and 0.2% (Day 0) or 0.5% (Day 1-3) (v/v) FBS (Corning). DMEM/F12 medium (Corning; 45000-350) was supplemented with 2% (v/v) FBS and 0.2% (w/v) NaHCO₃, and DMEM High Glucose medium (HyClone) was supplemented with 0.5X B-27™ supplement (Thermo Fisher Scientific). Human Activin A, mouse Wnt3a, human KGF, and human Noggin were purchased from R&D Systems. Other media components included TGFβ R1 kinase inhibitor IV (EMD Bioscience), KAAD-Cyclopamine (Toronto Research Chemicals), the retinoid analog TTNPB (Sigma Aldrich), the protein kinase C activator TPB (EMD Chemicals), the BMP type 1 receptor inhibitor LDN-193189 (Stemgent), and an inhibitor of the TGF-β type 1 activin like kinase receptor ALK5, ALK5 inhibitor II (Enzo Life Sciences).

Stage 1 (DE; collection on day 3):
Day 0: RPMI/FBS, 100 ng/mL Activin A, 25 ng/mL mouse Wnt3a
Day 1 – 2: RPMI/FBS, 100 ng/mL Activin A
Stage 2 (GT; collection on day 6):
Day 3: DMEM/F12/FBS, 2.5 µM TGFβ R1 kinase inhibitor IV, 50 ng/mL KGF
Day 4 – 5: DMEM/F12/FBS, 50 ng/mL KGF
Stage 3 (PP1; collection on day 10):
Day 6 – 9: DMEM/B27, 3nM TTNPB, 0.25 mM KAAD-Cyclopamine, 50 ng/mL Noggin
Stage 4 (PP2; collection on day 13):
Day 10 – 12: DMEM/B27, 100 nM ALK5 inhibitor II, 100 nM LDN-193189, 500 nM TPB, 50 ng/mL Noggin
Stage 5 (endocrine cell stage; collection on day 16):
Day 13 – 15: DMEM/B27, 100 nM ALK5 inhibitor II, 100 nM LDN-193189, 500 nM TPB, 50 ng/mL Noggin
For ribosome profiling experiments, a scalable suspension culture protocol was employed for differentiation of H1 cells to the PP2 stage (Rezania et al., 2014). Undifferentiated hESCs were aggregated and then maintained in mTeSR1 media (STEMCELL Technologies; supplemented with 10 µM Y-27632) at 1 x 10^5 cells/mL and overnight culture in six-well ultra-low attachment plates (Costar) with 5.5 ml per well on an orbital rotator (Innova2000, New Brunswick Scientific) at 100 rpm. The following day, undifferentiated aggregates were washed in MCDB 131 media (Thermo Fisher Scientific) and then differentiated using a multistep protocol with daily media changes and continued orbital rotation at either 100 rpm or at 115 rpm from days 8 to 14. In addition to 1% GlutaMAX™ ( Gibco) and 10 mM (days 0-10) or 20 mM (days 11-14) glucose, MCDB 131 media was supplemented with 0.5% (days 0-5) or 2% (days 6-14) fatty acid-free BSA (Proliant), 1.5 g/L (days 0-5 and days 11-14) or 2.5 g/L (days 6-10) NaHCO3 (Sigma-Aldrich), and 0.25 mM ascorbic acid (days 3-10).

Human Activin A, mouse Wnt3a, and human KGF were purchased from R&D Systems. Other media components included Insulin-Transferrin-Selenium-Ethanolamine (ITS-X; Thermo Fisher Scientific; days 6-10), retinoic acid (RA) (Sigma-Aldrich), the sonic hedgehog pathway inhibitor SANT-1 (Sigma-Aldrich), the protein kinase C activator TPB (EMD Chemicals), the BMP type 1 receptor inhibitor LDN-193189 (Stemgent), and the TGFβ type 1 activin like kinase receptor ALK5 inhibitor, ALK5 inhibitor II (Enzo Life Sciences).

To generate clonal lncRNA knockout hESC lines, combinations of pSpCas9(BB)-2A-Puro plasmid pairs (Addgene plasmid # 62988, gift from Feng Zhang) expressing Cas9 and single sgRNAs targeting upstream and downstream regions of the lncRNA promoter/locus were co-transfected into 1.5 x 10^6 H1 hESCs using the Human Stem Cell Nucleofector Kit 2 (Lonza) and the Amaxa Nucleofector II (Lonza). 24 hours after plating into Matrigel®-coated six-well plates, nucleofected cells were selected with puromycin (1 µg/mL mTeSR1 media) for 2-3 consecutive days. Individual colonies that emerged within 7 days after transfection were subsequently transferred manually into 96-well plates for expansion. Genomic DNA for PCR genotyping with GoTaq® Green Mastermix (Promega) and Sanger sequencing was then extracted using QuickExtract™ DNA Extraction Solution (Lucigen). The PDX1 knockout line was generated in an analogous way.

To generate sORF frameshift mutations, sgRNA sequences targeting the N-terminal region of the predicted small peptides were inserted into pSpCas9(BB)-2A-GFP (Addgene plasmid #48138, gift from Feng Zhang) via its BpiI cloning sites. 3 µg of the resulting plasmids were then transfected into 500,000 H1 cells plated into Matrigel®-coated six-wells the day prior, using XtremeGene 9 Transfection Reagent (Sigma-Aldrich) according to the manufacturer's instructions. 24 hours post-transfection, 10,000 GFP+ cells were sorted on an Influx™Cell Sorter (BD Biosciences) into Matrigel®-coated six-wells containing 1 mL mTeSR1 media supplemented with 10 µM ROCK inhibitor and 1X penicillin/streptomycin. Seven days after sorting, emerging colonies were hand-picked and transferred into 96-well plates for genotyping. Frame-shifts inside the targeted sORFs were confirmed by PCR-amplification of the sORF sequence with GoTaq® Green Mastermix and subsequent subcloning the PCR products into pCR2.1 (Thermo Fisher Scientific). For each hESC clone, at least six pCR2.1 clones were Sanger sequenced. Oligonucleotide sequences for sgRNA cloning are provided in Table S5A.

PCR genotyping of CRISPR clones
Four days after transfer of single cell-derived clones into 96-wells, cell culture supernatants containing dead cells were collected from each well prior to the daily media change. Cell debris was then pelleted and used for gDNA extraction with 10-20 µl QuickExtract™DNA Extraction Solution (Lucigen) according to the manufacturer's instructions. 1 µg DNA was then PCR-amplified with GoTaq® Green Mastermix (Promega) and locus-specific primers that anneal either within or outside of the excised genomic DNA. PCR products generated with "inside" primers were visualized on a 2% agarose gel, PCR bands generated with primers flanking the deletion were gel-purified and submitted for Sanger sequencing (see Table S5B for genotyping and sequencing primers).

For genotyping of sORF frameshift clones, PCR amplicons designed to encompass the Cas9 cut site were amplified and Sanger sequenced (Table S5B). If out-of-frame indels were apparent in the sequencing chromatogram, the sequenced PCR product was ligated into pCR2.1-TOPO via TOPO-TA cloning. A minimum of six clones were Sanger sequenced in order to determine the genotype at both alleles with high confidence.

Generation of sORF translation reporter plasmids
The four IncRNAs tested were PCR-amplified with KOD Xtreme™DNA Hotstart Polymerase (Millipore) from their 5' end up until the last codon of the sORF to be tested, omitting its stop codon (primer sequences are listed in Table S5D). cDNA was used as PCR template for LINC00261 and LHFPL3-AS2: RP11-834C11.4, and MIR7-3HG were amplified from a gBlock synthetic gene fragment (Integrated DNA Technologies; see Table S5F). The GFP coding sequence (without start codon; amplified from pRRLSIN.cPPT.PGK-GFP.WPRE) was then fused in-frame to the sORF via overlap extension PCR.
The resulting fusion product was cloned into pRRLSIN.cPPT.PGK-GFP.WPRE via BshTI and SalI restriction sites included in the PCR primers. Due to the 3'-location of sORF7 within LINC00261, not the entire LINC00261 cDNA was amplified but only 65 bp preceding sORF7.

To create the RP11-834C11.4-sORF-1XFLAG reporter construct in an analogous way, a gBlock synthetic gene fragment encompassing the FLAG-tagged sORF served as PCR template (Table S5F). The resulting PCR product was cloned into pRRLSIN.cPPT.PGK-GFP.WPRE via BshTI and SalI restriction sites.

**Generation of LINC00261 wild type and ∆ATGsORFS1-7 expression plasmids**

The LINC00261 wild type cDNA was PCR-amplified from pENTR/D-TOPO-LINC00261 (gift from Leo Kurian) with KOD Xtreme™ DNA Hotstart Polymerase (Millipore). Following the resulting PCR product was inserted into pRRLSIN.cPPT.PGK-GFP.WPRE via its appended BshTI/Sall cloning sites. Full-length LINC00261 ∆ATGsORFS1-7 was assembled through overlap extension PCR from the following three fragments and subsequently cloned into pRRLSIN.cPPT.PGK-GFP.WPRE via appended BshTI/Sall cloning sites: (i) a 1,248 bp PCR product amplified from a synthetic gene construct (Genewiz; see Table S5F for sequence) in which the ATG start codons of sORFs 1-6 had been mutated (ATG AAG / ATT / AGG / AAG / ATA / AGG), and (ii-iii) 3,111 bp/610 bp PCR fragments (amplified from the LINC00261 cDNA) in which the sORF7 start codon was mutated (ATG AAG). The obtained plasmids were sequence-verified by Sanger sequencing.

**Immunofluorescence staining**

H1 hESC-derived cells grown as monolayer on Matrigel®-coated coverslips were washed twice with PBS and then fixed with 4% paraformaldehyde in PBS for 30 min at room temperature. Following three washes in PBS, samples on coverslips were permeabilized and blocked with Permeabilization/Blocking Buffer (0.15% π(v/v) Triton X-100 and 1% normal donkey serum in PBS) for 1 hour at room temperature. Primary and secondary antibodies were diluted in Permeabilization/Blocking Buffer. Sections were incubated overnight at 4°C with primary antibodies, and then secondary antibodies for 30 min at room temperature. The following primary antibodies were used: rabbit anti-OCT4 (Cell Signaling Technology, 1:500), goat anti-SOX17 (Santa Cruz Biotechnology, 1:250), goat anti-FOXA2 (Santa Cruz Biotechnology, 1:250), goat anti-GATA6 (Santa Cruz Biotechnology, 1:50), guinea pig anti-insulin (Dako). Secondary antibodies (1:1000) were Cy3-, Cy5-, Alexafluor488-conjugated antibodies raised in donkey against guinea pig, rabbit, mouse, or goat (Jackson Immuno Research Laboratories). Images were acquired on a Zeiss Axio-Observer-Z1 microscope with a Zeiss AxioCam digital camera, and figures prepared with Adobe Photoshop/Illustrator CS5.

**Flow cytometry analysis**

For intracellular flow cytometry, single cells were washed three times in FACS buffer (0.1% π(w/v) BSA in DPBS) and then fixed and permeabilized with Cytotip/Cytoperm Fixation/Permeabilization Solution (BD Biosciences) for 20 min at 4°C, followed by two washes in BD Perm/Wash™ Buffer. Cells were next incubated with either PE-conjugated anti-SOX17 antibody (BD Biosciences), or PE-conjugated anti-INS antibody (Cell Signaling Technology) in 50 µl BD Perm/Wash™ Buffer for 60 min at 4°C. Following three washes in BD Perm/Wash™ Buffer, cells were analyzed on a FACSCanto II (BD Biosciences) flow cytometer.

**Insulin content measurements**

To measure total insulin content of endocrine cell stage control and IncRNA KO cells, adherent cultures were enzymatically detached from a 24-well at day 16 of differentiation. Upon quenching with FACS buffer (0.1% π(w/v) BSA in DPBS), the cells were pelleted and extracted over night at 4°C in 100 µl acid-ethanol (2% HCl in 80% ethanol). Insulin was measured by Insulin ELISA (Alpco) and normalized to total protein, as quantified with a BCA protein assay (Thermo Fisher Scientific).

**Quantitative reverse transcription PCR (qRT-PCR)**

Total RNA was isolated from hESC-derived cells and HEK293T cells using either TRIzol® (Thermo Fisher Scientific) or the RNeasy Mini Kit (Qiagen), respectively. Upon removal of genomic DNA (TURBO DNA-free Kit or RNase-free DNase Set) cDNA was synthesized using the iScript™ cDNA Synthesis Kit (Bio-Rad). PCR reactions were run in triplicate with 6.25-12.5 ng cDNA per reaction using the CFX96 Real-Time PCR Detection System (BioRad). TATA-binding protein (TBP)TM cDNA was synthesized using the iScript cDNA Synthesis Kit (Bio-Rad). PCR reactions were run in triplicate with 6.25-12.5 ng cDNA per reaction using the CFX96 Real-Time PCR Detection System (BioRad). TATA-binding protein (TBP)TM cDNA was synthesized using the iScript cDNA Synthesis Kit (Bio-Rad). PCR reactions were run in triplicate with 6.25-12.5 ng cDNA per reaction using the CFX96 Real-Time PCR Detection System (BioRad). TATA-binding protein (TBP)TM Set) cDNA was synthesized using the iScript cDNA Synthesis Kit (Bio-Rad). PCR reactions were run in triplicate with 6.25-12.5 ng cDNA per reaction using the CFX96 Real-Time PCR Detection System (BioRad). TATA-binding protein (TBP)TM cDNA was synthesized using the iScript cDNA Synthesis Kit (Bio-Rad). PCR reactions were run in triplicate with 6.25-12.5 ng cDNA per reaction using the CFX96 Real-Time PCR Detection System (BioRad). TATA-binding protein (TBP)TM

**Reduced Serum Medium (Thermo Fisher Scientific) followed by brief vortexing. After five minutes, the transfection complex was ultracentrifuged for 2 hours at 19,400 rpm using an Optima L-80 XP Ultracentrifuge (Beckman Coulter).

**Transient transfection of HEK293T cells with polyethylenimine (PEI)**

Two hours prior to transfection, fresh pre-warmed DMEM medium (Corning) was added to each well. Transfection mix was prepared by combining PEI and plasmid DNA (4:1 ratio; 4 µg PEI per 1 µg DNA) in Opti-MEM™ Reduced Serum Medium (Thermo Fisher Scientific) followed by brief vortexing. After five minutes, the transfection complex was added dropwise to the cells.

**Lentivirus preparation and ectopic LINC00261 expression**

Lentiviral particles were prepared by co-transfecting HEK293T cells (using PEI) with the pCMVR8.74/pMD2.G helper plasmids and with pRRLSIN.cPPT.PGK-GFP.WPRE transfer plasmid, in which the GFP ORF had been replaced with the 4.9 kb LINC00261 cDNA. Virus-containing supernatant was collected for two consecutive days and concentrated by ultracentrifugation for 2 hours at 19,400 rpm using an Optima L-80 XP Ultracentrifuge (Beckman Coulter). To express LINC00261 (wild type) and LINC00261 (∆ATGsORFS1-7) in HEK293T cells, the cells were plated in 6-well plates and transduced with lentivirus the following day. Two days post infection, the cells were passaged for RNA half-life
**LINC00261 RNA half-life measurement**

HEK293T cells transduced with either LINC00261 (wild type) or LINC00261 (ΔATG) lentivirus were seeded in six 24-wells. 48 hours after plating, cells from one well were collected for RNA isolation as the “0 hour” time point. To the remaining five wells, 100 µl growth media supplemented with 10 µg/ml actinomycin D were added to inhibit transcription. At 2, 4, 6, 8, and 9 hours following actinomycin D addition, samples were collected for RNA isolation. Total RNA was then reverse transcribed and analyzed by qPCR, where the abundance of each time point was calculated relative to the abundance at the 0 hour time point (ΔCt). The half-life was then determined by non-linear regression (One phase decay; GraphPad Prism).

**Single molecule RNA fluorescence in situ hybridization (smRNA FISH)**

H1-derived PP2 stage cells (control and LINC00261 KO) were cultured on Matrigel®-coated 12 mm diameter coverslips in a 24-well plate. Following 10 min fixation in 1 ml Fixation Buffer (3.7 % (v/v) formaldehyde in 1X PBS) at room temperature, the cells were washed twice in PBS and subsequently permeabilized in 70 % (v/v) ethanol for one hour at 4 °C. Following a five minute wash in Stellaris RNA FISH Wash Buffer A (LGC Biosearch Technologies; 1:5 dilution concentrate, with 10% (v/v) formamide added), the coverslips were incubated in a humidified chamber at 37 °C for 14 hours with probes diluted in Stellaris RNA FISH Hybridisation Buffer (LGC Biosearch Technologies; with 10% (v/v) formamide added) to 125 nM. After a 30 min wash at 37 °C in Wash Buffer A, the cells were counter-stained with Hoechst 33342 (Thermo Fisher Scientific) for 15 min and washed in RNA FISH Wash Buffer B (LGC Biosearch Technologies) for 5 min at room temperature. The coverslips were mounted in Vectashield Mounting Medium (Vector Laboratories) and imaged on a UltraView Vox Spinning Disk confocal microscope (PerkinElmer) using a 100X oil objective.

**In vitro transcription/translation of IncRNAs**

Synthetic gene constructs containing complete transcript isoforms (including the predicted 5’ and 3’ UTR) of four translated IncRNAs (RP11-834C11.4, LINC00261, MIR7-3HG, and LHFPL3-AS2) were produced by Genewiz (constructs available upon request). Microproteins were translated in vitro from 0.5 µl linearized plasmid DNA using the TnT® Coupled Wheat Germ Extract System (Promega) in the presence of 10 mM/mL [35S]-methionine (Hartmann Analytic) according to manufacturer’s instructions. 5 µl lysate was denatured for 2 min at 85 °C in 9.6 µL Novex Tricine SDS Sample Buffer (2X) (Thermo Fisher Scientific) and 1.4 µL DTT (500 mM). Proteins were separated on 16% Tricine gels (Thermo Fisher Scientific) for 1 h at 50 V followed by 3.5 h at 100 V and blotted on PVDF-membranes (Immobilon-PSQ Membrane, Merck Millipore). Incorporation of [35S]-methionine into newly synthesized proteins enabled the detection of translation products by phosphor imaging (exposure time of 1 day).

**In vivo translation assays**

Reporter plasmids were transfected into HEK293T cells using PEI, and 36 hours post transfection live cells were imaged on an EVOS Cell Imaging System (Thermo Fisher Scientific) equipped with a 20X objective. Additional constructs were generated that served as negative controls (no GFP fluorescence):

1) a LINC00261-sORF3-GFP construct with a single ‘T’ insertion inside sORF3, causing a frame-shift,
2) a LINC00261-sORF2-GFP construct with a stop codon preceding the GFP coding sequence, and
3) a LINC00261-sORF1-GFP construct with a frame-shift mutation within the GFP coding sequence.

**Stranded mRNA-seq library preparation for IncRNA KOs**

Total RNA from PP2 cells differentiated with the Rezania et al. (2012) protocol was isolated and DNase-treated using either TRIzol® (Thermo Fisher Scientific), or the RNAeasy Mini kit (Qiagen) according to the manufacturer’s instructions. RNA integrity (RIN >8) was verified on the Agilent 2200 TapeStation (Agilent Technologies), and 400 ng RNA was used for multiplex library preparation with the KAPA mRNA HyperPrep Kit (Roche). All libraries were evaluated on TapeStation High Sensitivity DNA ScreenTapes (Agilent Technologies) and with the Qubit dsDNA High Sensitivity (Life Technologies) assays for size distribution and concentration prior to pooling the multiplexed libraries for single-end 1x51nt or 1x75 sequencing on the HiSeq4000 instrument.

**Cell fractionation and ribo-minus RNA-seq**

H1 hESCs were differentiated to the PP2 stage with the Rezania et al. (2012) protocol, then nuclear and cytosolic RNA was isolated with the Paris™ Kit (Thermo Fisher Scientific). Unfractionated total RNA was set aside as a control. All samples were DNase-treated prior to further processing (TURBO DNA-free™ Kit; Thermo Fisher Scientific). rRNA-depleted total RNA-seq libraries were prepared with TruSeq® Stranded Total RNA Library Prep Gold (Illumina), and sequencing was performed on a HiSeq4000 instrument.

**Alignment of IncRNA KO mRNA-seq samples and processing for gene expression analysis**

Using the Spliced Transcripts Alignment to a Reference (STAR) aligner (STAR 2.5.3b; (Dobin et al., 2013)), sequence reads were mapped to the human genome (hg38/GRCh38) with the Ensembl 87 annotations in 2-pass mapping mode, allowing for up to 6 mismatches. Cufflinks (part of the Cufflinks version 2.2.1 suite (Trapnell et al., 2010; Roberts et al., 2011)), was then used to quantify the abundance of each transcript cataloged in the Ensembl 87 annotations in reads per kilobase per million mapped reads (RPKM). For plotting expression values, a pseudocount of 1 was added to all RPKM...
values prior to log2-transformation.

Genes with RPKM \( \geq 1 \) across two replicates were deemed expressed. Differential gene expression was tested using the DESeq2 v1.10.1 Bioconductor package (Love et al., 2014) with default parameters. Input count files for DESeq2 were created with htsseq-count from the HTSeq Python library (Anders et al., 2015). Genes with a >2-fold change and an adjusted p-value of \(< 0.01\) were considered differentially expressed. The chromosomal localization of genes differentially expressed upon LINC00261 KO was visualized with the RCircos package in R (https://cran.r-project.org/web/packages/RCircos/index.html).

**LncRNA classifications**

The following transcript biotypes were grouped into the “lncRNA” classification: 3’ overlapping ncRNA, antisense, bidirectional promoter lncRNA, lincRNA, macro lncRNA, non coding, processed transcript, sense intronic, sense overlapping, TEC.

LncRNAs with \( \geq 1 \) RPKM during all differentiation stages of CyT49 hESCs (ES, DE, FG, GT, PP1, PP2) were categorized as constitutively expressed (“constitutive”), whereas lncRNAs with \(< 1 \) RPKM throughout differentiation were considered “never expressed”. LncRNAs expressed in at least one of the stages (but not in all five stages) were referred to as dynamically expressed (“dynamic”). Furthermore, for each lncRNA, its maximum RPKM value was determined across 38 tissues/cell types (see “Gene-gene correlations and GO enrichment” section below). Log2-transformed maximum expression values (RPKM + pseudocount of 1) were graphed as boxplots for different gene sets using the ggplot2 R package (https://cran.r-project.org/web/packages/ggplot2/index.html). To determine the subcellular localization of IncRNAs, first all IncRNAs expressed in the nuclear and/or cytosolic RNA fraction (RPKM \( \geq 1 \) in two biological replicates) of H1-derived PP2 stage cells were selected. Among these expressed IncRNAs, those with \( \geq 1 \) RPKM\textsubscript{cytosol} and \(< 1 \) RPKM\textsubscript{nucleus} were classified as “cytosol enriched”. Conversely, lncRNAs with \(< 1 \) RPKM\textsubscript{cytosol} and \( \geq 1 \) RPKM\textsubscript{nucleus} were termed “nucleus enriched”. LncRNAs expressed in both fractions (\( \geq 1 \) RPKM\textsubscript{cytosol} and \( \geq 1 \) RPKM\textsubscript{nucleus}) were tagged with “both”.

**Assignment of IncRNAs to their nearest coding gene using GREAT**

GREAT (Genomic Regions Enrichment of Annotations Tool 3.0.0; (McLean et al., 2010)) was run with the “Single nearest gene” within 1000 kb option to assign the nearest coding genes to the following sets of lncRNAs: i) DE-transcribed lncRNAs, ii) PP2-transcribed lncRNAs that are not transcribed at the DE stage (non-transcribed control set for i)), iii) PP2-transcribed lncRNAs, and iv) lncRNAs transcribed at the DE stage but not transcribed in PP2 cells (non-transcribed control set for iii)). The log2-transformed RPKM values of the IncRNA-associated coding genes were then graphed as boxplots using ggplot2. The corresponding absolute coding-to-lncRNA inter-gene distances were visualized as cumulative frequency plots.

**Gene-gene correlations and GO enrichment**

Pearson correlations were calculated among all genes across a catalog of 38 tissues/cell types derived from all three germ layers (11 illumina BodyMap 2.0 tissues, other publicly available data sets (see “Data Sources” below), and EndoC-βH1 RNA-seq data generated in our lab). Scatter plots of the log2-transformed RPKM values for IncRNAs/neighboring TFs and histograms of the Pearson correlation coefficients were plotted in R using ggplot2.

Spearman correlations were calculated to test for expression correlation among all genes expressed (RPKM \( \geq 1 \)) in a minimum of ten out of 38 tissues. The resulting correlation matrix was then used to calculate the Euclidean distance followed by hierarchical clustering. The resulting heatmap was subdivided into ten clusters. Cluster visualization was done using heatmap.3 (https://raw.githubusercontent.com/obigriffith/biostar-tutorials/master/Heatmaps/heatmap.3.R) from ggplot v3.0.1 (http://cran.r-project.org/web/packages/ggplot2/index.html). GO enrichment (Ashburner et al., 2000; The Gene Ontology, 2019) and KEGG pathway (Kanehisa et al., 2017) analyses to assign functional annotation to all ten clusters were performed with gProfiler v0.6.4 (Reimand et al., 2016) using g:Profiler archive revision 1741 (Ensembl 90, Ensembl Genomes 38).

**Alignment and processing of ChIP-seq samples**

All sequence reads were filtered to include only those passing the standard Illumina quality filter, and then aligned to the Homo sapiens reference genome (hg38/GRCh38) using Bowtie version 1.1.1 (Langmead et al., 2009). The following parameters were used to select only uniquely aligning reads with a maximum of two mismatches:

```
-k 1 -m 1 -l 50 -n 2 -best -strata
```

SAMtools (Li et al., 2009) was then used to filter reads with a MAPQ score less than 30 and to remove duplicate reads. Finally, replicate ChIP-seq and input BAM files were merged and sorted. The HOMER makeUCSCfile function (Heinz et al., 2010) was used to create a bedGraph formatted file for viewing in the UCSC Genome Browser.

**Ribosome profiling and matching RNA-seq**

Ribosome profiling was performed on PP2 cells obtained from six independent differentiations of H1 hESCs with the Rezania et al. (2014) protocol, yielding an average of 89% PD1X-positive cells. Ribosome footprinting and sequencing library preparation was done with the TruSeq® Ribo Profile (Mammalian) Library Prep Kit (Illumina) according to the TruSeq® Ribo Profile (Mammalian) Reference Guide (version August 2016). In short, 50 mg of PP2 aggregates were washed twice with cold PBS and lysed for 10 minutes on ice in 1mL lysis buffer (1 x TruSeq Ribo Profile mammalian...
polysome buffer, 1 % Triton X-100, 0.1% NP-40, 1 mM dithiothreitol, 10 U ml-1 DNase I, cycloheximide (0.1 mg/ml) and nuclease-free H2O). Per sample, 400 µL of lysate was further processed according to manufacturer’s instructions. Final library size distributions were checked on the Bioanalyzer 2100 using a High Sensitivity DNA assay (Agilent Technologies), multiplexed and sequenced on an Illumina HiSeq 4000 producing single end 1x51 nt reads. Ribo-seq libraries were sequenced to an average depth of 85M reads.

Total RNA was isolated using TRIzol® Reagent (Thermo Fisher Scientific) from the exact same cell cultures processed for ribosome profiling (10% of the total number of cells). Total RNA was DNase treated and purified using the RNA Clean & Concentrator™-25 kit (Zymo Research). RIN scores (RIN = 10 for all 6 samples) were measured on a BioAnalyzer 2100 using the RNA 6000 Nano assay (Agilent Technologies). Poly(A)-purified mRNA-seq library preparation was performed according to the TruSeq Stranded mRNA Reference Guide (Illumina), using 500 ng of total RNA as input. Libraries were multiplexed and sequenced on an Illumina HiSeq 4000 producing paired-end 2x101 nt reads.

Alignment of Ribo-seq and matched mRNA-seq samples

Prior to mapping, ribosome-profiling reads were clipped for residual adapter sequences and filtered for mitochondrial, ribosomal RNA and tRNA sequences (Table S2). Next, all mRNA and ribosome profiling data were mapped to the Ensembl 87 transcriptome annotation of the human genome hg38 assembly using STAR 2.5.2b (Dobin et al., 2013) in 2-pass mapping mode. To avoid mRNA-seq mapping biases due to read length, 2x101 nt mRNA-seq reads were next trimmed to 29-mers, those mRNA reads were processed and mapped with the exact same settings as the ribosome profiling data. For the mapping of 2x101 nt RNA-seq reads 6 mismatches per read were allowed (default is 10), whereas 2 mismatches were permitted for the Ribo-seq and trimmed mRNA-seq reads. To account for variable ribosome footprint lengths, the start point of the read was defined using the option –seedSearchStartLmaxOverLread, which was set to 0.5 (half the read, independent of ribosome footprint length). Furthermore, –outFilterMultimapNmax was set to 20 and –outSAMmultNmax to 1, which prevents the reporting of multimapping reads.

Detecting actively translated reading frames

Canonical ORF detection using ribosome profiling data was performed with RiboTaper v1.3 (Calviello et al., 2016) with standard settings. For each sample, we selected only the ribosome footprint lengths for which at least 70% of the reads matched the primary ORF in a meta-gene analysis. Following the standard configuration of RiboTaper, we required ORFs to have a minimum length of 8aa, evidence from uniquely mapping reads and at least 21 P-sites. The final list of translation events was stringently filtered requiring the translated gene to have an average RNA RPKM ≥ 1 and to be detected as translated in all 6 profiled samples. Furthermore, we required the exact ORF to be detected independently in at least 4 out of 6 samples.

Translational efficiency estimates

Translational efficiency (TE) estimations were calculated as the ratio of Ribo-seq over mRNA-seq DESeq2 normalized counts, yielding independent gene-specific TEs for each of the 6 individual replicate differentiations. For this, mRNA-seq and Ribo-seq based expression quantification was calculated for (annotated and newly detected) coding sequences (CDSs / ORFs) only, using RNA reads trimmed to footprint sizes as described above.

Data sources

The following datasets used in this study were downloaded from the GEO and ArrayExpress repositories:

- RNA-seq: Illumina BodyMap 2.0 expression data from 16 human tissues (GSE30611); polyA mRNA RNA-seq from BE2C (GSE93448), GM12878 (GSE33480), 293T (GSE34995), HeLa (GSE33480), HepG2 (GSE90322), HUVEC (GSE33480), Jurkat (GSE93435), K562 (GSE33480), MiaPaCa-2 (GSE43770), Panc1 (GSE93450), PFSK-1 (GSE93451), U-87 MG (GSE90176); CyT49 hESC/DE/GT/PP1/PP2 (E-MTAB-1086). ChiP-seq: H3K4me3/H3K27me3 in CyT49 hESC/DE/GT/PP1/PP2 (E-MTAB-1086).

Statistical analyses

Statistical analyses were performed using Microsoft Excel, GraphPad Prism (7.05), and R (v.3.5.0). Statistical parameters such as the value of n, mean, standard deviation (S.D.), standard error of the mean (S.E.M.), significance level (*p < 0.05, **p < 0.01, ***p < 0.001 and ****p < 0.0001), and the statistical tests used are reported in the figures and figure legends. The “n” refers to the number of independent pancreatic differentiation experiments analyzed (biological replicates), or the number of genes/transcripts and sORFs detected. Statistically significant gene expression changes were determined with DESeq2.

Data availability

All mRNA-seq and Ribo-seq datasets generated for this study have been deposited at GEO under the accession number GSE144682.


Supplemental Information

Title: A functional screen of translated pancreatic lncRNAs identifies a microprotein-independent role for LINC00261 in endocrine cell differentiation

Inventory:

I. Supplemental Data

Figure S1, Related to Figure 1
Figure S2, Related to Figure 2
Figure S3, Related to Figure 3
Figure S4, Related to Figure 4

Table S1 - Related to Figure 1. Identification, regulation, and characterization of lncRNAs during pancreatic differentiation. (A) Gene expression during pancreatic differentiation (RPKM). (B) lncRNA-proximal TFs, by cluster in correlation heatmap (Figure S1H). (C) GO enrichment and KEGG pathway analysis for each cluster in the correlation heatmap (Figure S1D).
(supplied as Excel file: Table S1.xlsx)

Table S2 - Related to Figure 2. RNA-seq after subcellular fractionation and Ribo-seq in PP2 cells. (A) Subcellular fractionation of PP2 stage cells (RPKM). (B) Ribo-seq/mRNA-seq contaminant filtering statistics, read size distribution, and Pearson correlation coefficients of all sequenced Ribo-seq and polyA RNA-seq libraries. (C) All ORFs detected by RiboTaper, including lncRNA sORFs. (D) lncRNA sORFs detected by RiboTaper and conservation statistics (PhyloCSF scores). (E) Translation efficiency calculations.
(supplied as Excel file: Table S2.xlsx)

Table S3 - Related to Figure 3. Differentially expressed genes after lncRNA deletion. (A) Coordinates of CRISPR deletions. (B) Differentially expressed genes in GATA6-AS1 knockout at definitive endoderm stage. (C) Differentially expressed genes in GATA6-AS1 knockout at definitive endoderm stage. (D) Differentially expressed genes in LINC00261 knockout at definitive endoderm stage. (E) Differentially expressed genes in LINC00617 knockout at PP2 stage. (F) Differentially expressed genes in GATA6-AS1 knockout at PP2 stage. (G) Differentially expressed genes in LINC00479 knockout at PP2 stage. (H) Differentially expressed genes in RP11-834C11.4 knockout at PP2 stage. (I) Differentially expressed genes in SOX9-AS1 knockout at PP2 stage. (J) Differentially expressed genes in MIR7-3HG knockout at PP2 stage. (K) Differentially expressed genes in LHFP3-AS2 knockout at PP2 stage.
(supplied as Excel file: Table S3.xlsx)

Table S4 - Related to Figure 4. Characterization of LINC00261 knockout and LINC00261-sORF3-frameshift PP2 cells. (A) Differentially expressed genes in LINC00261 knockout PP2 stage cells. (B) Sequences of LINC00261 wild type and frameshift mutants. (C) Differentially expressed genes in LINC00261-sORF3-frameshift PP2 stage cells.
(supplied as Excel file: Table S4.xlsx)

Table S5 List of oligonucleotides and synthetic gene fragments used in this study. (A) sgRNA oligonucleotides used for cloning into PX458/Px459. (B) Genotyping and sequencing primers for KO validation. (C) qRT-PCR primers. (D) Cloning primers (translation reporter constructs and lentiviral LINC00261 overexpression plasmids). (E) Synthetic gene fragments. (F) Custom LINC00261 Stellaris® RNA FISH probe set.
(supplied as Excel file: Table S5.xlsx)
Figure S1. Related to Figure 1. Characterization of IncRNAs expressed during pancreatic differentiation. (A,B) Left: Expression of the single nearest coding genes (± 1000 kb) in cis to transcribed and non-transcribed IncRNAs at the DE stage (A) or PP2 stage (B). Log2 transformed mean expression values (RPKM + pseudocount) from two biological replicates were used to generate the box plots (****, p-value < 0.0001, Wilcoxon rank sum test). Right: Corresponding cumulative distance distribution functions. (C) Heatmap of the hierarchically clustered expression correlations (Spearman’s rho) of all RNAs transcribed during pancreatic differentiation (with RPKM ≥ 1 in at least ten out of 38 tissues). Transcription factor (TF)-encoding mRNAs, IncRNAs (all), dynamically expressed IncRNAs (RPKM ≤ 1 in at least one stage (ESC to PP2)), and TF-proximal IncRNAs are highlighted above the heatmap. Clusters 8 and 10 are significantly enriched for all of these RNAs (*, p-value < 0.03, Fisher test). (D) Gene ontology and KEGG pathway analysis for all coding genes in cluster 8 (p-value < 0.05, Fisher test). The full list of significantly enriched terms is shown in Table S1C. (E-H) H3K4me3 and H3K27me3 ChIP-seq tracks of loci containing IncRNAs GATA6-AS1 (A), LINC00261 (B), PDX1-AS1/PLUTO (C), or SOX9-AS1 (D) during pancreatic differentiation of CyT49 hESCs.
Figure S2. Related to Figure 2. Cytosolic IncRNAs engage with ribosomes. (A) Venn diagrams showing the number of coding RNAs (left) and IncRNAs (right) with RPKM ≥ 1 across two biological replicates in cytosolic and nuclear factions. (B) Box plots of maximum IncRNA expression (RPKM + pseudocount) across 38 tissues binned by their degree of cytosolic localization (measured as nuclear/cytosolic IncRNA expression ratio deciles in PP2); the expression of all PP2-transcribed coding RNAs with dynamic expression during differentiation is included for reference. The pie chart summarizes the proportions of translated IncRNAs within each cytoplasmic localization decile. (C) Read length distribution (nt) of Ribo-seq fragments across replicate Ribo-seq experiments (n = 6 biological replicates). (D) Position of the inferred P-sites of the ribosome footprints relative to the reading frame of PP2-transcribed coding genes. (E-F) Coverage of 29 nt footprint P-sites around the start codons (E) or stop codons (F) of PP2-transcribed coding genes. (G) Box plots comparing maximum expression of translated and untranslated IncRNAs (RPKM + pseudocount) across 38 tissues (****, p-value = 2.12x10-8, Wilcoxon rank sum test). For the untranslated set, 285 untranslated PP2-expressed IncRNAs were selected randomly. (H) Density plots comparing the translation efficiencies of PP2-expressed mRNAs and IncRNAs. (I) Autoradiograph of radiolabeled in vitro translation products derived from full-length LHFPL3-AS2, MIR7-3HG, LINC00261, and RP11-834C11.4. EV, empty vector. (J) Anti-FLAG immunofluorescence staining of HEK293T cells transiently transfected with a PGK-RP11-834C11.4-sORF-1xFLAG construct. (K) Microphotograph of HEK293T cells transiently transfected with a PGK-LINC00261-sORF4-GFP construct with mitochondria labeled by MitoSOX Red. (L) Golgi immunofluorescence staining (anti-GM130) of HEK293T cells transiently transfected with a PGK-LINC00261-sORF7-GFP construct. Scale bars = 10 µm.
Figure S3. Related to Figure 3. Minor gene expression changes in definitive endoderm or pancreatic progenitor cells after lncRNA deletion. (A) Genome Browser snapshots of RNA-seq signal at the indicated lncRNA loci in control (ctrl) and lncRNA knockout (KO; -/-) DE (green tracks) and PP2 (red tracks) stage cells. Genomic deletions are indicated by gray boxes. (B) Bar graphs showing expression of indicated lncRNAs in control and lncRNA KO DE (green) and PP2 (red) cells quantified by RNA-seq. Data are shown as mean RPKM ± S.D. (n = 2 independent differentiations of two independent KO clones, except for SOX9-AS1 for which one clone was differentiated twice). (C) Volcano plots displaying gene expression changes in control versus lncRNA KO DE (green) or PP2 (red) cells. Differentially expressed genes (DESeq2; > 2-fold change (FC), adjusted p-value < 0.01; vertical and horizontal dashed lines indicate the thresholds; n = 2 independent differentiations of two independent KO clones, except for SOX9-AS1 for which one clone was differentiated twice) are shown in green (DE) and red (PP2). TF genes in cis to deleted lncRNAs are shown in gray (gray dots represent genes with ≤ 2-fold change and/or adjusted p-value ≥ 0.01).
Figure S4. Related to Figure 4. Characterization of LINC00261-deleted pancreatic progenitor cells (A) RNA-seq expression heatmap of LINC00261 across 35 cell types/tissues originating from all three germ layers (shown as RPKM + pseudocount). (B) Heatmap showing K-means clustering of 108 differentially expressed genes (DESeq2; > 2-fold change (FC), adjusted p-value < 0.01) between PP2 cells from control (ctrl) and LINC00261−/− H1 hESCs (based on expression z-score; n = 6 independent differentiations). (C) Top: Genome Browser snapshot of RNA-seq signal at the LINC00261/FOXA2 locus in control and LINC00261−/− PP2 stage cells. Genomic deletions are indicated by gray boxes. Bottom: Bar graphs showing LINC00261 and FOXA2 expression in control and LINC00261−/− PP2 cells quantified by RNA-seq. Data are shown as mean RPKM ± S.D. (n = 6 independent differentiations of four independent KO clones). ****, p-value < 0.0001; NS, p-value > 0.05; t-test. (D) LINC00261 smRNA FISH in control and LINC00261−/− PP2 cells. Scale bars = 8 µm. (E) qRT-PCR analysis of LINC00261 (top) and INS (bottom) expression in control and LINC00261-sORF-FS H1 hESC clones at the endocrine cell (EC) stage. Data are shown as mean ± S.E.M. (n ≥ 3 independent differentiations for each clone).